

Blast Result



Blast 2 Sequences results

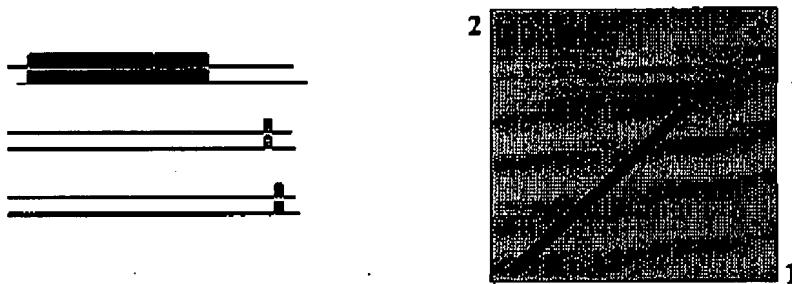
PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.16 [Mar-25-2007]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2
x\_dropoff: 0 expect: 10.0000 wordsize: 11 Filter View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
Show CDS translation Align

Sequence 1: lcl|seq\_1
Length = 4867 (1 .. 4867)

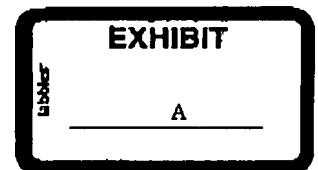
Sequence 2: lcl|seq\_2
Length = 4936 (1 .. 4936)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

[Redacted sequence header]



Score = 3012 bits (1566), Expect = 0.0
Identities = 2570/3067 (83%), Gaps = 6/3067 (0%)
Strand=Plus/Plus

Query 357 TGGGCGAGGGCTGTCCTCAGAAGCTGGTGACTGCTAACTTGCTGCGCTTCCTCCTGCTGG 416
Sbjct 189 TGGGCAATGGCTGCTCTCAGAAGCTGGCGACTGCTAACCTCCTCCGGTTCCTATTGCTGG 249
Query 417 TGCTCATCCCCTGCATCTGCGCCCTCATCGTGCTGCTGGCCATCCGCTGTCTTTGTGG 476
Sbjct 249 TCCTGATTCCATGTATCTGTGCTCTCGTTCTCTTGCTGGTGATCCTGCTTCCTATGTTG 308
Query 477 GAACATTAAAAAGGGTTTATTCAAATCAAATGACAGTGAACCTTTGGTCACTGATGGGG 536
Sbjct 309 GAACATTACAAAAGGTCTATTTAAATCAAATGGGAGTGAACCTTTGGTCACTGATGGTG 368





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Query	2337	GTGTGACCCCTCTCTAAAAATGGGAACCTCTCTCATTGCTGACTGTTTCAAAAATCTGCAA	2396
Sbjct	2166	GTGTGACCCCTCTCTATAAATGTGAACTCCTCTTCTTCTGATGGTTTACAGAGCTGCCA	2225
Query	2397	AGGAACACCACGTGTGTGCTGACGGCTGGCGGGAGACGTTGAGTCAGCTGGCCTGCAAGC	2456
Sbjct	2226	CAGAACACCATGTGTGTGTCAGATGGCTGGCAGGAGATATTGAGTCAGCTGGCCTGCAAGC	2285
Query	2457	AGATGGGTTTAGGAGAACCCTCTGTGACCAAGCTGATCCCAGGACAGG---AAGGCCAGC	2513
Sbjct	2286	AGATGGGTTTAGGAGAACCATCTGTGACCAAATTGATACAGGAACAGGAGAAAGAGCCGC	2345
Query	2514	AGTGGCTGAGGTTGTACCCCAACTGGGAGAATCTCAATGGGAGCACCTTGCAGGAGCTGC	2573
Sbjct	2346	GGTGGCTGACATTACACTCCAACCTGGGAGAGCCTCAATGGGACCACTTTACATGAACTTC	2405
Query	2574	TGGTATACAGGCCTCTGCCCCAAGCAGAAGTGAGATTTCCCTTCTGTGCTCCAAGCAAG	2633
Sbjct	2406	TAGTAAATGGGCAGTCTTGTGAGAGCAGAAGTAAATTTCTCTTCTGTGTACTAAACAAG	2465
Query	2634	ACTGTGGCCGCGCCCTGCTGCCCCGAATGAACAAGAGGATCCTTGGGGGTCGGACTAGTC	2693
Sbjct	2466	ACTGTGGCCGCGCCCTGCTGCCCCGAATGAACAAAAGGATCCTTGGAGGTCGGACGAGTC	2525
Query	2694	GTCTGGGAGGTTGGCCGTGGCAGTGTCTCTGTCAGAGTGAACCCAGTGGACATATCTGTG	2753
Sbjct	2526	GCCCTGGAAGGTTGGCCATGGCAGTGTCTCTGTCAGAGTGAACCCAGTGGACATATCTGTG	2585
Query	2754	GCTGTGTCCTCATTGCCAAGAAGTGGGTCTGACAGTTGCCCATGCTTTGAAGGGAGAG	2813
Sbjct	2586	GCTGTGTCCTCATTGCCAAGAAGTGGGTCTGACAGTTGCCCATGCTTTGAGGGGAGAG	2645
Query	2814	AAGACGCTGATGTTTGGAAAGTGGTATTTGGCATAAACAACCTGGACCATCCATCAGGCT	2873
Sbjct	2646	AGAATGCTGCAGTTTGGAAAGTGGTGCTTGGCATCAACAATCTAGACCATCCATCAGTGT	2705
Query	2874	TCATGCAGACCCGCTTTGTGAAGACCATCCTGCTACATCCCCGTTACAGTCGAGCAGTGG	2933
Sbjct	2706	TCATGCAGACACGCTTTGTGAAGACCATCATCCTGCATCCCCGCTACAGTCGAGCAGTGG	2765
Query	2934	TAGACTATGATATCAGCGTGGTGGAGCTGAGCGATGATATCAATGAGACAAGCTACGTCA	2993
Sbjct	2766	TGGACTATGACATCAGCATCGTTGAGCTGAGTGAAGACATCAGTGAGACTGGCTACGTCC	2825
Query	2994	GACCTGTCTGCCTACCCAGTCCGGAGGAGTATCTAGAACCAGATACGTACTGCTACATCA	3053
Sbjct	2826	GGCCTGTCTGCTTGGCCAACCCGGAGCAGTGGCTAGAGCCTGACACGTACTGCTATATCA	2885
Query	3054	CAGGCTGGGGCCACATGGGCAATAAAATGCCCTTTAAGCTGCAGGAGGGAGAGGTCCGCA	3113
Sbjct	2886	CAGGCTGGGGCCACATGGGCAATAAAATGCCATTTAAGCTGCAAGAGGGAGAGGTCCGCA	2945
Query	3114	TTATCCCTCTGGAGCAGTGCCAGTCTTATTTTGCATGAAGACCATCACCAATCGGATGA	3173
Sbjct	2946	TTATTTCTCTGGAACATTGTCACTCTACTTTGCATGAAGACCATCACCACTCGGATGA	3005
Query	3174	TCTGTGCTGGCTATGAGTCTGGCACCGTGGACTCCTGCATGGGAGACAGCGGTGGGCCTC	3233
Sbjct	3006	TATGTGCTGGCTATGAGTCTGGCACAGTTGATTTCATGCATGGGTGACAGCGGTGGGCCTC	3065



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PubMed

Entrez

BLAST

OMIM

Taxonomy

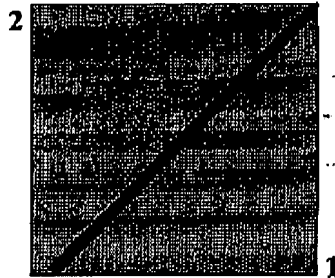
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.16 [Mar-25-2007]

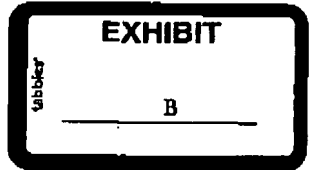
Matrix: BLOSUM62 gap open: 11 gap extension: 1
x\_dropoff: 0 expect: 10.000 wordsize: 3 Filter View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
Show CDS translation Align

Sequence 1: lcl|seq\_1
Length = 1113 (1 .. 1113)

Sequence 2: lcl|seq\_2
Length = 1042 (1 .. 1042)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.



Score = 1658 bits (4293), Expect = 0.0, Method: Composition-based stats.
Identities = 849/1023 (82%), Positives = 921/1023 (90%), Gaps = 2/1023 (0%)

Table with 4 columns: Query, Sbjct, alignment, and score. It lists multiple sequence alignments with their respective scores and identities.

Blast Result

Query	326	SLOQEHGKQSLCGGGSFLCTSGLCVPPKLLQCNGYNDCCDDWSDEAHCNCSKDLFHC GTGK	385
Sbjct	258	SQQE+GKQ LCG GE+FLC SG+C+P KLQCNGYNDCCDDWSDEAHCNCS++LFHC TGK	
Query	386	CLHYSLLCDGYDDCGDPSDEQNCDCNLTKEHRCGDGRCIAAEWVCDGDHDCVDKSDEVNC	445
Sbjct	318	CL+YSL+CDGYDDCGD SDEQNCDCN T EHRCGDGR CIA EWVCDGDHDCVDKSDEVNC	377
Query	446	SCHSQGLVECTSGQCIPSTFQCDGDEDCKDGSDEENCSDSQTCPPEGEQCGFGSSCVESC	505
Sbjct	378	SCHSQGLVECTSGQCIPSTFQCDGDEDCKDGSDEENCSDSQTCPPEGEQCGFGSSCVESC	437
Query	506	AGSSLCDSDSSLSNCSQCEPITL ELCMNL LNHTHPNYLGHRTQKEASISWESSLFPAL	565
Sbjct	438	GSSLCD++SL+NCSQCEPITL ELCMNL LNHTHPNYLGHRTQKEASISWESSLFPAL	497
Query	566	VQTNKYKYLMMFFACTILVPKCDVNTGQRIPPCRLLCEHSKERCESVLGIVGLQWPEDTDC	625
Sbjct	498	VQTNKYKYLMMFFACTILVPKCDVNTGQRIPPCRLLCEHSKERCESVLGIVGLQWPEDTDC	557
Query	626	NQFPPESSDNQTCLLPNEDVEECSPSHFKCRSGRCVLSRRCDGQADCDSDSDEENC	685
Sbjct	558	+QFPPE+SDNQTCL+P+E VEECSPSHFKCRSG+CVL SRRCDGQADCDSDSDEENC	617
Query	686	ERALWECFPFNKQCLKHTLICDGFPPDCPDSMDEKNCSFCQDNELECANHECVPRDLWCDGW	745
Sbjct	618	ERDLWECFPFNKQCLKHTVICDGFPPDCPDSMDEKNCSFCQDNELECANHECVPRDLWCDGW	677
Query	746	VDCSDSSDEWGCVTLSKNGNSSLLTVHKSABEHVHCADGWRETLSQLACKQMGLEPSV	805
Sbjct	678	ADCSDSSDEWGCVTLSINVNSSSFLMVHRAATEHVCADGWRETLSQLACKQMGLEPSV	737
Query	806	TKLIPQEQGQ-QWLRLYPNWENLNGSTLQELLVYRHSCPSRSEISLLCSKQDCGRRPAAR	864
Sbjct	738	TKLIQE+WL L+ NWE+LNG+TL ELLV SC SRS+ISLLC+KQDCGRRPAAR	797
Query	865	MNKRILGGRTSRPGRWPWQCSLQSEPSGHICGCVLIACKWVLTVAHCFEGREDADVWKVV	924
Sbjct	798	MNKRILGGRTSRPGRWPWQCSLQSEPSGHICGCVLIACKWVLTVAHCFEGRENAAVWKVV	857
Query	925	FGINNLDHPSGFMQTRFVKTIILHPRYSRAVDYDISVELSDDINETSIVRVPVCLPSP	984
Sbjct	858	GINNLDHPSGFMQTRFVKTIILHPRYSRAVDYDISVELSDDINETSIVRVPVCLPSP	917
Query	985	EYLEPDTYCYITGWGHMGNKMPFKLQEGEVRIIPLEQCOSYFDMKTIITRNICAGYESGT	1044
Sbjct	918	QWLEPDTYCYITGWGHMGNKMPFKLQEGEVRIIPLEQCOSYFDMKTIITRNICAGYESGT	977
Query	1045	VDSCMGDSGGPLVCE+PGG+WTLFGLTWSGVCFSKVLGPGVYSNVSYFVGVIERQIYIQ	1104
Sbjct	978	VDSCMGDSGGPLVCEKPGGRWTLFGLTWSGVCFSKVLGPGVYSNVSYFVGVIERQIYIQ	1037
Query	1105	TFL 1107	
Sbjct	1038	TFL 1040	

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.